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The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services

<130> 015280-382100PC

<141> 2001-05-29

<151> 1998-11-30

<151> 1999-11-24

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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tgcctccgag cgcacgcate ctgagatcct gagcctttgg ttaagaccga gctctattaa 180

gctgaaaaga taaaaactct ccag atg tct tcc agt aat gtc gaa gtt ttt 231

Met Ser Ser Ser Asn Val Glu Val Phe

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atc cca gtg tca caa gga aac acc aat ggc ttc ccc gcg aca gtt tcc 279

Ile Pro Val Ser Gln Gly Asn Thr Asn Gly Phe Pro Ala Thr Val Ser

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aat qac ctg aaq qca ttt act gaa gga gct gtg tta agt ttt cat aac 327

Asn Asp Leu Lys Ala Phe Thr Glu Gly Ala Val Leu Ser Phe His Asn

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atc tgc tat cga gta aaa ctg aag agt ggc ttt cta cct tgt cga aaa 375

Ile Cys Tyr Arg Val Lys Leu Lys Ser Gly Phe Leu Pro Cys Arg Lys

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Pro Val Glu Lys Glu Ile Leu Ser Asn Ile Asn Gly Ile Met Lys Pro	
60 65 70	
ggt ctc aac gcc atc ctg gga ccc aca ggt gga ggc aaa tct tcg tta	471
Gly Leu Asn Ala Ile Leu Gly Pro Thr Gly Gly Gly Lys Ser Ser Leu	
75 80 85	
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Leu Asp Val Leu Ala Ala Arg Lys Asp Pro Ser Gly Leu Ser Gly Asp	
90 95 100 105	
gtt ctg ata aat gga gca ccg cga cct gcc aat ttc aaa tgt aat tca	567
Val Leu Ile Asn Gly Ala Pro Arg Pro Ala Asn Phe Lys Cys Asn Ser	
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Gly Tyr Val Val Gln Asp Asp Val Val Met Gly Thr Leu Thr Val Arg	
125 130 135	
gaa aac tta cag ttc tca gca gct ctt cgg ctt gca aca act atg acg	663
Glu Asn Leu Gln Phe Ser Ala Ala Leu Arg Leu Ala Thr Thr Met Thr	
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aat cat gaa aaa aac gaa cgg att aac agg gtc att gaa gag tta ggt	711
Asn His Glu Lys Asn Glu Arg Ile Asn Arg Val Ile Glu Glu Leu Gly	
155 160 165	
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Leu Asp Lys Val Ala Asp Ser Lys Val Gly Thr Gln Phe Ile Arg Gly	
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gtg tct gga gga gaa aga aaa agg act agt ata gga atg gag ctt atc	807
Val Ser Gly Gly Glu Arg Lys Arg Thr Ser Ile Gly Met Glu Leu Ile	
190 195 200	
act gat cct tcc atc ttg tcc ttg gat gag cct aca act ggc tta gac	855
Thr Asp Pro Ser Ile Leu Ser Leu Asp Glu Pro Thr Thr Gly Leu Asp	
205 210 215	
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Ser Ser Thr Ala Asn Ala Val Leu Leu Leu Leu Lys Arg Met Ser Lys	
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cag gga cga aca atc atc ttc tcc att cat cag cct cga tat tcc atc	951
Gln Gly Arg Thr Ile Ile Phe Ser Ile His Gln Pro Arg Tyr Ser Ile	
235 240 245	
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Phe Lys Leu Phe Asp Ser Leu Thr Leu Leu Ala Ser Gly Arg Leu Met	
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Phe His Gly Pro Ala Gln Glu Ala Leu Gly Tyr Phe Glu Ser Ala Gly	
270 275 280	
tat cac tgt gag gcc tat aat aac cct gca gac ttc ttc ttg gac atc	1095
Tyr His Cys Glu Ala Tyr Asn Asn Pro Ala Asp Phe Phe Leu Asp Ile	
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Ile Asn Gly Asp Ser Thr Ala Val Ala Leu Asn Arg Glu Glu Asp Phe	
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aaa gcc aca gag atc ata gag cct tcc aag cag gat aag cca ctc ata	1191
Lys Ala Thr Glu Ile Ile Glu Pro Ser Lys Gln Asp Lys Pro Leu Ile	
315 320 325	
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Glu Lys Leu Ala Glu Ile Tyr Val Asn Ser Ser Phe Tyr Lys Glu Thr	
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aaa gct gaa tta cat caa ctt tcc ggg ggt gag aag aag aag aag atc	1287
Lys Ala Glu Leu His Gln Leu Ser Gly Gly Glu Lys Lys Lys Lys Ile	
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Thr Val Phe Lys Glu Ile Ser Tyr Thr Thr Ser Phe Cys His Gln Leu	
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Arg Trp Val Ser Lys Arg Ser Phe Lys Asn Leu Leu Gly Asn Pro Gln	
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gcc tct ata gct cag atc att gtc aca gtc gta ctg gga ctg gtt ata	1431
Ala Ser Ile Ala Gln Ile Ile Val Thr Val Val Leu Gly Leu Val Ile	
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ggg gcc att tac ttt ggg cta aaa aat gat tct act gga atc cag aac	1479
Gly Ala Ile Tyr Phe Gly Leu Lys Asn Asp Ser Thr Gly Ile Gln Asn	
410 415 420 425	
aga gct ggg gtt ctc ttc ttc ctg acg acc aac cag tgt ttc agc agt	1527
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Val Ser Ala Val Glu Leu Phe Val Val Glu Lys Lys Leu Phe Ile His	
445 450 455	
gaa tac atc agc gga tac tac aga gtg tca tct tat ttc ctt gga aaa	1623
Glu Tyr Ile Ser Gly Tyr Tyr Arg Val Ser Ser Tyr Phe Leu Gly Lys	
460 465 470	
ctg tta tct gat tta tta ccc atg agg atg tta cca agt att ata ttt	1671
Leu Leu Ser Asp Leu Leu Pro Met Arg Met Leu Pro Ser Ile Ile Phe	
475 480 485	
acc tgt ata gtg tac ttc atg tta gga ttg aag cca aag gca gat gcc	1719
Thr Cys Ile Val Tyr Phe Met Leu Gly Leu Lys Pro Lys Ala Asp Ala	
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Phe Phe Val Met Met Phe Thr Leu Met Met Val Ala Tyr Ser Ala Ser	
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 Thr Leu Leu Met Thr Ile Cys Phe Val Phe Met Met Ile Phe Ser Gly
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 555 560 565

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 570 575 580 585

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cct tgt aac tat gca aca tgt act ggc gaa gaa tat ttg gta aag cag 2055
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gct tgt atg att gtt att ttc ctc aca att gcc tac ctg aaa ttg tta 2151
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ttt ctt aaa aaa tat tct taaatttccc cttaattcag tatgatttat 2199
 Phe Leu Lys Lys Tyr Ser
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tgttcccttg ccatcacact gttgcacagc agcaattggt ttaaagagat acatttttag 2319

aaatcacaac aaactgaatt aaacatgaaa gaaccacaaga catcatgtat cgcataattag 2379

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ggtttgccat tatttaatat atgacaaatg tattaatgct atactggaaa tgtaaaattg 2619

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<213> Homo sapiens

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 35 40 45
 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
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 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
 65 70 75 80
 Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
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 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
 100 105 110
 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Asp Asp
 115 120 125
 Val Val Met Gly Thr Leu Thr Val Arg Glu Asn Leu Gln Phe Ser Ala
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 Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
 145 150 155 160
 Ile Asn Arg Val Ile Glu Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
 165 170 175
 Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
 180 185 190
 Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Ser
 195 200 205
 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
 210 215 220
 Leu Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
 225 230 235 240
 Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
 245 250 255
 Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
 260 265 270
 Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
 275 280 285
 Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
 290 295 300
 Val Ala Leu Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu
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 Pro Ser Lys Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr
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09856927-09160

Val Asn Ser Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu
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 370 375 380
 Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile
 385 390 395 400
 Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu
 405 410 415
 Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe
 420 425 430
 Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe
 435 440 445
 Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr
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 Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro
 465 470 475 480
 Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met
 485 490 495
 Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr
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 Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys
 530 535 540
 Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr
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 Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr
 565 570 575
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 Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys
 595 600 605
 Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp
 610 615 620
 Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe
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 Ile Ala Thr Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr
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 atc gct ttt gta ttt atg atg ctc ttt tct ggc ctc ttg gtg aat ctc 144
 Ile Ala Phe Val Phe Met Met Leu Phe Ser Gly Leu Leu Val Asn Leu
 35 40 45
 aga acc att ggg cct tgg ctg tcc tgg ctt cag tac ttt agc att cct 192
 Arg Thr Ile Gly Pro Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro
 50 55 60
 cga tat ggc ttc aca gct ttg cag tat aat gaa ttc ttg gga caa gag 240
 Arg Tyr Gly Phe Thr Ala Leu Gln Tyr Asn Glu Phe Leu Gly Gln Glu
 65 70 75 80
 ttt tgt cca gga ttc aat gta acg gac aac agc act tgt gtt aac agc 288
 Phe Cys Pro Gly Phe Asn Val Thr Asp Asn Ser Thr Cys Val Asn Ser
 85 90 95
 tat gca ata tgt act ggt aac gag tac ttg ata aat cag ggc atc gaa 336
 Tyr Ala Ile Cys Thr Gly Asn Glu Tyr Leu Ile Asn Gln Gly Ile Glu
 100 105 110
 ctg tca cct tgg gga ctg tgg aag aat cat gtg gcc ctg gct tgt atg 384
 Leu Ser Pro Trp Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met
 115 120 125
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 Ile Ile Ile Phe Leu Thr Ile Ala Tyr Leu Lys Leu Leu Phe Leu Lys
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 35 40 45

Arg Thr Ile Gly Pro Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro
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Arg Tyr Gly Phe Thr Ala Leu Gln Tyr Asn Glu Phe Leu Gly Gln Glu
 65 70 75 80

Phe Cys Pro Gly Phe Asn Val Thr Asp Asn Ser Thr Cys Val Asn Ser
 85 90 95

Tyr Ala Ile Cys Thr Gly Asn Glu Tyr Leu Ile Asn Gln Gly Ile Glu
 100 105 110

Leu Ser Pro Trp Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met
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Lys Tyr Ser
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<213> Artificial Sequence

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